

SEQ.I.D.NO:31

1 GTAAGAAAGG CATTGCAAG AGATTGTGGC TGCTTATTTT GCCGCCCCCT
51 TCCGACGGGC CCGCCGGGGG TAGCTGAGAG GCCCACCAGG GTTGCGGGAG
101 AAACCGAACC GGGTGGGGGG AGGGTCCGAC TTGGAGGGGC GAGGGGGAAG
151 ACCCACGGCC GACGCGGCCA CCAGGTCGAG GCGGAGGGTA GGGACAGCCC
201 GGCTAGGGTC AGGCGTGCGA GGTCTGTTAC GAGGCCTCGA CCCGAGGCGG
251 TGCCATGCGC GAAGCCCCGG CGCTGAGTGG CGAGACGGGG TCGCGACCTG
301 GCGTGGGAAA GAAAGGTGGA GGCGGCCGCC ACTATGTGTG GCCCAGAGCC
351 GGCAGGTCCG GTTGCCCTCC TGTGCCGGGG GAGGGACGGC GCGCGGGGTT
401 CCGGAGCATT CTGACGGTAC CACTCGCGAG AGGCGGGGGT GCCTGGTCCT
451 TAGATCCAGT CACTTCGTCT CGGCTAAAAC ACGGGTCGGG GAGAAGAAAC
501 CGGCCGTTCA GTGTGCTGGT TTTCTTGACG GCCAGGACTG AGCCTAACCC
551 CGAGGAGCGG CCGCGTGAGG CACCAGGAGC CCACCCGGCG CCGGGCGGGC
601 GGGTCCATTT TGCCGCACAA GCCGGGCTAT TGGCAAAGTG CGGATGGGCA
651 GGTCCACCTT CCTTCGGGGG TGAGCGGCCT GAGGTATGGG AGGGCGACGC
701 TACTTCGCGA CGGGGGCGGG CGGGATGTGG ATTGTTCCAT GGAGGGGTGG
751 GAGACRCCGC CGGGTGGTCG ARGGAGCGAG CACATGGTGG CCTGAGGCGT
801 TCCCCTCCCC CAGTCTGCTT CGCTTCTAAG TGTTGTGCAA TCTCCCCCTT
851 TGCTAGCTCG GCTTGGGCTC ATTGTGCGCG AGGCCGCCAC CGCCCGCGGC
901 CTCCACATC CGGGCAACGC GAGGGGGGGG CTTCGGCTGG AGGGAGTGGG
951 GGAGGGCGCG GGCGGGATGA CGTGGGGGGA AGGGGATGTC CTACCCTCCG
1001 ATCTGGGAGG TGAAGGGCGG GACTTCCAGC GCGCTGGTGC TGCGGTGGGA
1051 GGTGCACGCG CTTGGGCTTT AAGCGGCTGG GTCGGGCCCA CGTGGACCCG
1101 GCGGCAAGCA CCACCTNTGG GCACCGTGAG CGCGGCGGCA CGCCTGCCGG
1151 CCTGTCTTCA GAAAGGGTCA CCCCCTTATG TCGGGGGTGG CCTGGCCTGA

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1201 GCCGCTGCCT GCATGGGGCA AATGCCTCAG TTTTATAGAA ACTCCTCCTT
1251 TGGGTATTTT TTGGGAGCTG GTGGGAGTTG GATCTGGGAC AGCAGGTTGA
1301 TGGCATCATG CAGGCCACTC CTGACAGAGC CCGGCTGTCA GGATTTCTGA
1351 GTGCTTCGGT CGGGCAGGGG ACAAACTTA TGCTTTAAAC CAACAG

SEQ.I.D.NO:32

1 GTGAGACTGG AGAAATGGAA TTCTGTCCTC CCCCATTACA ACTTTCAGCC
51 GTATAGAGTT AGAGTGGCCT CTTGATTGAT TTCCCAGATC ATCTAGAAGC
101 AGCTGGTTTC CCTAAAGGGA GGAGGGTTGT AAGCTCTGAG GCTTTTGTTA
151 RTASGCACCA SATTCTGTTT GCTCGGAGAC TACAGCTCAG CTCCACCTTT
201 TCCATGACTC AAGCTTTAAT TTCTTTGCAT CCCCTAG

SEQ.I.D.NO:33

1 GTGAGACCTC TCAGTCCCAG ATGCCCATCT CATATCAGCC AGGGACAAAG
51 CAACTCCTTG TTCATCCCAG CTTGGCTTTT GATCCGTGCC CATGCCTGGT
101 TCATGCCTTG GACACATAGG TTTCCTTTAA AGAGGTGGTA TTGTAGCCAG
151 CTTATATTTG CATCTACAGC CATGTTTCTA GTCCAGCTTG GTGTGCAATA
201 CTAGATGAGT TAATAACTGG TCCTTGTTTC TGATCTGGTT CCCATTGTGT
251 AACTGTGTTG ATTGGGAAGG TAGTTTGTGA GCCATGAAAT GCTTG GTTCA
301 TTGGTTGCTT ATTGACCTCA TTAACCTAGG ACTTGAATAT CCCAAAGGGT
351 ATGCTCTTTA CCACATTCAA CTCCTAATTT ATTTGTTTAG

SEQ.I.D.NO:34

1 GTGAGTAATT CGGTTCTCCA ATCCCCTGGG TCACTTTGCT CTTGTGCACG
51 CTTTCCAGTC TTTCAGCGTA AGCCAGAGTC ATTCCCAAGG ATGCTGGTTT
101 CTCTCTGGGG GAAGAGCTGC TCTGTGATGG AGCCCATGCG TGTCATCTGA
151 GCCTCTGGCT TCCCTGCCAG TGCAGCCCTG GCAGTGTCTT ACTTCCCAGG
201 GCTGTTGTCT GCCTGGCGGG AAGGTCCTGG GCAAAGGATC AGTCTTTGTA
251 CTCTGAGAGC AGACTACTTG GCTCCTCTCT GTTTTTTATC AGCGAAGTTG
301 GATATATCTC TCCCACATTT CCCTAATCAT ATGCTATATA TTGGCTTTTT
351 TTTTCTTCTC TAG

SEQ.I.D.NO:35

1 GTGAGGGCAG TCTTGCTTGA ATAGCTAATG ATTCTTGAAA AATAGTAAGT
51 GCCAGGGGAA ACCAAATACT GGATTCTTGA GCCTTTTAT GCATCTGCTT
101 CAGTTTTAGG TGTGGCTAGG GAAGGGAGCA GGCCTCAGGA AGGAACCAGC
151 ACTCTAAGAC TGGCCTTTTT TTCCACTAG

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SEQ.I.D.NO:36

1 GTGGGGCCCA GTGCAGGAGG CGGGCCTGGT AGTGAGTTGT TGGGTATAGC
51 CCCTGACTGA TTTTGTCCC CCAACCTCCA G

SEQ.I.D.NO:37

1 GTGAGTAGAG GGAAGTATA GCAAAGGCAG AAGGGAGGAT CCAAGGTGAT
51 TCCCTCTCCA AGGGGACATC AGTGCCTCTC AGGAAAGTAG CAGCTTGGAA
101 TAGAATCTGG CATGCCTAAG GCCTTTGGGG AACTGGGATG CTTATTTCTT
151 CTGCCTTCCT TGGCTGCCCA CATGGATGCC TAAGTGTCTT CCCTCCGGGA
201 TAGAGTGTCC TCCGTGCACA TGCTGAAGAG TTGTCTTTCT TGACGTAG

SEQ.I.D.NO:38

1 CTACGATATC GCTGTTGATT TCCTTCATCC CCTGGCACAC GTCCAGGCAG
51 TGTCGAATCC ATCTCTGCTA CAGGGGAAAA ACAAATAACA TTTGAGTCCA
101 GTGGAGACCG GGAGCAGAAG TAAAGGGAAG TGATAACCCC CAGAGCCCGG
151 AAGCCTCTGG AGGCTGAGAC CTCGCCCCC TTGCGTGATA GGGCCTACGG
201 AGCCACATGA CCAAGGCACT GTCGCCTCCG CACGTGTGAG AGTGCAGGGC
251 CCCAAGATGG CTGCCAGGCC TCGAGGCCTG ACTCTTCTAT GTCACTTCCG
301 TACCGGCGAG AAAGGCGGGC CCTCCAGCCA ATGAGGCTGC GGGGCGGGCC
351 TTCACCTTGA TAGGCACTCG AGTTATCCAA TGGTGCCTGC GGGCCGATGT
401 CTGCGAGCCA GGATTCCCG

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SEQ.I.D.NO:39

-526 CTACGATATC GCTGTTGATT TCCTTCATCC CCTGGCACAC GTCCAGGCAG
-476 TGTCGAATCC ATCTCTGCTA CAGGGGAAAA ACAAATAACA TTTGAGTCCA
-426 GTGGAGACCG GGAGCAGAAG TAAAGGGAAG TGATAACCCC CAGAGCCCCGG
-376 AAGCCTCTGG AGGCTGAGAC CTCGCCCCCC TTGCGTGATA GGGCCTACGG

c-ets1

Sp1

-326 AGCCACATGA CCAAGGCACT GTCGCCTCCG CACGTGTGAG AGTGCAGGGC
-276 CCCAAGATGG CTGCCAGGCC TCGAGGCCTG ACTCTTCTAT GTCACCTCCG

c-ets/Elk-1

-226 TACCGGCGAG AAAGGCGGGC CCTCCAGCCA ATGAGGCTGC GGGGCGGGCC

Sp1

-176 TTCACCTTGA TAGGCACTCG AGTTATCCAA TGGTGCCTGC GGGCCGGAGC

AP-2

-126 GACTAGGAAC TAACGTCATG CCGAGTTGCT GAGCGCCGGC AGGCGGGGCC

CRE-BP

AP-2

Sp1

-76 GGGGCGGCCA AACCAATGCG ATGGCCGGGG CGGAGTCGGG CGCTCTATAA

Sp1

Sp1

-26 GTTGTCGATG GGCGGGCACT CCGCCCTAGT TTCTAAGGAT CATGTCTGCG

metserala

+24 AGCCAGGATT CCCG

serglnasp ser

SEQ.I.D.NO:40

-5280 GCGGCCGCAT AATACGACTC ACTATAGGGA TCTAGGAAGG CCTCTCATAG
 -5230 CTGAGACGTG AATGATGAGC AGCCAGCCAT GCGCAGACCT GGAATAGCA
 -5180 AGTACACAAG ACCCATAGTG AAAAACCATG GCTGAGGAAC AGAGGGCTTG
 -5130 TGGGGGTGAC CTGTGTAGTT GGCGCAGAGT GAGCAAAGGG AGATGGATAC
 -5080 AAAATTCGGT CAGAGAGTAG ATCATGTAAG ACATGTACGG TAGGCTGAGG
 -5030 AGGGGGGATT TTATTGCGTG TATACTGAGA AGCCATTGAG TTTAAGCAG
 -4980 GCTGAGAAGT GCCTTCTGTT TTAAACTCCT GTTCAATGA CAGATTGAAA
 -4930 GGGGGGCAAG AATGGAAGCA GGAACAGAGC ACAGTAGTCC AGGTGAGAAA
 -4880 CTTGAACTGG AGTGCTAAAG GAAGAGAGAG AGAGTAGTTT TATGTAGGAT
 -4830 AAATTTTACG AGTAAAACCA GTAGGACTGA CAGGCTCTGT GATACTGAGA
 -4780 GATACATATT TGTCTCCTGA CCAGGCTCCT GGCATTCAAC TTCTAAAATC
 -4730 CTTGGAATCT CCAGTGATGT GTGTTTTTGT GTGCTGATGA GTTGATTCAT
 -4680 GGCTAGCCCC TCTAGGTGGC TTCATGATTA GAGGGTTGGA ACTTTCAGCC
 -4630 TCACCCCCAC CAACTTCCTG GGAGGGGAAT GGGGCCAAAG GTAAAGGCAA
 -4580 TCAGTGAGGA TCAGTGATTT AATCAGTCAT GCCTAGTAGT GAAGCCTCTA
 -4530 AAAACCGGAA AGGGGCCGGG TTGCGCGGCG CACGCCTGTA CTCCCGGCAC
 -4480 TTTGGGAGGC TGAGGCAGAT GGATCGCAAG GTCAAGAGAT TGAGACCAGC

Alu I repeat

-4430 CTGGCCGACC TGGCGAAACC CTGTCTCTAC TAAAAATATG AAAATTAGCT
 -4380 GGGCGTGGTG CGTGCGCCTG TAGTCCCCGG GAGGCTGAGG CAGGAGAATC
 -4330 GCTTGAACCC GGGAGGCAGA GGTTCAGTG AGCCGAGATT GTGCCACTGC
 -4280 ACTCCACCCT GGGTGACAGA GTGAACTCT GTCTCAAAAA AGAAAAAAAAA
 -4230 ACCCGAGAGG AGGAGTTTGG AGACATTCTA GATAGCTGAA GGCATGGAGG
 -4180 CTGCCACAG GATGGTCTGC CAGGCCTCTT CCCGGTACCT TTCCCTGTGC

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-4130 ATCTTTTCAT CTGTACTCTT TGTACTACCC TTTGTTAATA AACTGGTAAA
-4080 TGTGTTTCCA TGAGTTCTGT GAGCTGCTCT AACAAATTAA TCAAATTCAA
-4030 GGAGGGGGTC ATGGGAACGC TGATCTAACC AGTTGGTGAG AAACACAGAT
-3980 AAAACAACCT GGGGCTTACG ACTGGCATCA GAATTGGGGG CAGCCTTG TG
-3930 AGACTGAGCC CTAAACCTGT GACACATTAT CTCCAGGTAG ATAGTGTGG
-3880 AATTGAATTG GGGGATACCC AGCTGTGTCC ACCGCAAAT TGCTTGCTTG
-3830 GTTGTTGGTG GAGAGAAAGC CCCACAAACA CTTCTTGGTG ACCACAGGTT
-3780 ACAGAAGTAT TTTGTGTTGT GAGAGTATAG TAGGAAAGAA GATTTGTTTT
-3730 TTTGCCGGGC GCGGTGGCTC ACGCCTGTAA TCCCAGCCCT TTGGGAGGCT
-3680 GAGGCGGGCG GATCACCAGG TCAGGAGATC AAGACCATCC TGGCTAACAC
-3630 AGTGAAACCC TGTCTCTACT AAAAATACAA AAAATTAGCC GGGCGAGGTG

Alu I repeat

-3580 GCACGTGTCT GTAGTCCAAG CTACTTGGGA GGCTGAGGCA GGAGAATGGC
-3530 ATGAACCCAG GAGGTGGAGC TTGCAGTGAG GCAAGATCAC GCCACTGCAC
-3480 TCCAGTCTGG GCAACAGAGC AAGACTCCGT CTCAAAAAA AAAAAAAAAA
-3430 AAAAGATTG TTTTTCCTC TGCAGGTTGG ATGTGGGAAA TGAAGAAAAA
-3380 GAAATGGAGG ATGATGCCTA GGTTTTTGGC CTATGTAACG GGAAAAAGTGG
-3330 GAGAGGAACA GGTTGGGGGA GGAAAATGAA GAGTCTTTT CTCTTCTGGT
-3280 TTCCCTGCCC TCCCATTCAA AAGCCAGGAA ATTTCTACAG CTAGGCAGGA
-3230 TGATTGGCTC CGGCATTCCCT TAATTTTCAGT CCTCAAAATC AAGAGCTTAC
-3180 ACCCTCAGGG ATCTTCTTGC AGTAGAGGGA AGGGTGGTGA CGTACAGTGA
-3130 AAAACATGTT GGCCTTCTTC ATACTGAGTT TGAGTCCCAC TTCTGCCATT
-3080 TCTTTCTTTC ATGACCTTGT GCAAGTCACG ACTTTCCAAG CTGCAATTTT
-3030 CTCATCTGTT AGGTTGAATG TTGAGAACTT CCCGGTAGGA TTGTTATGAG
-2980 CATTAACTGC GTGTTTACTT TGTGCTGTGT CTTGTTCTAA GTGTATTATG
-2930 GATAGTCACT AGTTTAATCC TCATATCAAA TGGATGAGGT GTAGGTACTA
-2880 CTATTTACAC TCTCTGACAG ATAAGGAAAC TGAGGTATAG AAGGTTATTA

-2830 AGTAGGTTGC CCACTGTCAT AAGCCAGTAA ATGGAGGAGC TGTATTTGAA
-2780 TTCTGGCAGG CTCCAGAATC CTGGGCCTGG GTTCTTAGCT GCTAAGTGCT
-2730 TCTCCCTTTA AAGTGTGAAA AGCGCCTGCC CATCATGGGT TCTCAAGTGT
-2680 TCGTTCTGAT GTCTCCTCCA TTGTCTGACC TTCCTCCCTT ACCCCGAAGA
-2630 ACCGAAACAT GCAGATCCTG AGCTTGCCCA CAATCTAGGC CTTGGGTCTT
-2580 CTGTTCTTTC ACTTG GTTCC CTTACCTGTG TCTCTGTTCC TCTCTAGAAC
-2530 CTTTCATGGCA AAAGGCAAGA CTTCTGTTTG TTGTACCTGA CCTGTGGCAC
-2480 TATCTCTTTA GGTGGACATC TTCAATAAGG AGCTACTGCT AATCCCCATC
-2430 CACCTGGAGG TGCATTGGTC CCTCATCTCT GTTGATGTGA GCGGACGCAC
-2380 CATCACCTAT TTTGACTCGC AGCGTACCCT AAACCGCCGC TGCCCTAAGG
-2330 TTTGAGGGGG TAGGAGAGAG ATGGGCAAAA TGTGGGGCGG TGCAGTGGCA
-2280 AGGCATTGCA GGAAGAAGGG TGGGCTTTGG GTCTTTGAGG GCGGACCTGG
-2230 GCATGGTGTC TGCCAGCACT GTACCCACCA TACTGTGTTC AATTGAGAAA
-2180 CTTAGGGCAT CACTTTCTTT TCCCCATCC ACATAGCATA TTGCCAAGTA
-2130 TCTACAGGCA GAGGCGGTAA AGAAAGACCG ACTGGATTTC CACCAGGGCT
-2080 GGAAAGGTTA CTTCAAAATG GTGAGTTTCC TGAGGGAGGG GTATAGGGTG
-2030 TTGGTGGGGA CAGTGGTAGA AGGCAGAAAT TGAAGTCCTA CCCCTGGGAG
-1980 TCTCCATGTG AAGGGCCTGC TTTCTTTCTC TTCTCTAGAA TGTGGCCAGG
-1930 CAGAATAATG ACAGTGA CTG TGGTGCTTTT GTGTTGCAGG TAAGCAGATG
-1880 ATGGGGCCAC CTCCTCTAGC TCTGAAGTCA GTTGGGTAA AGGGTCGGGA
-1830 GGCTGTTATG CATCCCCCTCA TTTGGCTCAT AGTCAGTTGT GGAGCAGGAA
-1780 GTAATCTGTT TTAGAACACC AAAACACTGG CTTCACTGGT TCTCTTCTGG
-1730 ACTTCTCCAT CCCACATTGG GACTGGGTCT CTAGGTCTTT TGGCTCTGGC
-1680 CTTTCATAGAG CTCCTGCTA ACCTCCA ACT CAGTGTATTT TCTCCATCTA
-1630 AAACATTCTA TCAAGTAAGA AACTAGCTT TAGAGTCAGG CTGTTTTTGA
-1580 ACCCCAGGCT GTGGGACCCT GGCTCCCTTT GGGGATGTTT TCTGAAGGAT
-1530 GGAGACACAT CTCATATGAA ATGTGTAGCA CAGGTCCTGA CACGGGGGGT

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-1480 TTCTCATGGC TTGCTTTGTT AACACCCAGT ACTGCAAGCA TCTGGCCCTG
 -1430 TCTCAGCCAT TCAGCTTCAC CCAGCAGGAC ATGCCCAAAC TTCGTCGGCA
 -1380 GATCTACAAG GAGCTGTGTC ACTGCAAAC TACTGTGTGA GCCTCGTACC
 -1330 CCAGACCCCA AGCCCATAAA TGGGAAGGGA GACATGGGAG TCCCTTCCCA

Homology to mouse eIF4A gene sequence

-1280 AGAAACTCCA GTTCCTTTCC TCTCTGCTT CTTCCCACTC ACTTCCCTTT
 -1230 GGTTTTTCAT ATTTAAATGT TTCAATTTTCG TGTATTTTTT TTTCTTTGAG
 -1180 AGAATACTTG TTTATTTCTG ATGTGCAGGG GATGGCTACA GAAAAGCCCC
 -1130 TTTCTTCCTC TGTTTGCAGG GGAGTGTGGC CCTGTGGCCC TGGGTGGAGC
 -1080 AGTCATCCTC CCCCTTCCCC GTGCAGGGAG CAGGAAWTCA GNGATGGGGG
 -1030 GNGGGGGGCG GACAATAGGA TNACAGCCCG CCAGATATNC ATATATATAT
 -980 ATATATATAT ATATATATAT ATATATATAT ATATATATAT ATATATATAT
 -930 ATATATATAT ATATATAAAA ATGCCACGGT CCTGCTCTGG TCAATAAAGG
 -880 ATCCTTTGTT GATACGTAAG TGGTGGTCTT CCTTAAGGGG CTTCAAATTA
 -830 GTGGATATGC TTAGCTCAGA CCTTCCAGCC AGTNTCTTGA GACTAAAGGG
 -780 TTCAGCTTTC CATCCCTGGC TCAGGCACTG CCAACACCTT GTCTTCACCC
 -730 AAACAAATCC CCCAGATGGG AGCAGAGAGC AGGAAGGAGG GAAAGTAGAT
 -680 AAGCCTCAAG AATAAGGGCA TCCGAGAGGG AAGCGTGGGG AACTGGACAC
 -630 AAGGGACTGG GGAGGGGACC AACCAGGATT CATGATAGTA CCCCCAAGCC
 -580 CTTTACAGTT TTYTTCCATC CCTCCACCAT CCAGCCAGGG GAATCCTCCC
 -530 ATCCCTACGA TATCGCTGTT GATTTCTTTC ATCCCTGGC ACACGTCCAG
 -480 GCAGTGTGCA ATCCATCTCT GCTACAGGGG AAAAACAAT AACATTTGAG
 -430 TCCAGTGGAG ACCGGGAGCA GAAGTAAAGG GAAGTGATAA CCCCCAGAGC
 -380 CCGGAAGCCT CTGGAGGCTG AGACCTCGCC CCCCTTGCCT GATAGGGCCT
 -330 ACGGAGCCAC ATGACCAAGG CACTGTCGCC TCCGCACGTG TGAGAGTGCA
 -280 GGGCCCCAAG ATGGCTGCCA GGCCTCGAGG CCTGACTCTT CTATGTCACT
 -230 TCCGTACCGG CGAGAAAGGC GGGCCCTCCA GCCAATGAGG CTGCGGGGCG

15

Homology to mouse eIF4A gene sequence

-180 GGCCTTCACC TTGATAGGCA CTCGAGTTAT CCAATGGTGC CTGCGGGCCG
-130 GAGCGACTAG GAACTAACGT CATGCCGAGT TGCTGAGCGC CGGCAGGCGG
-80 GGCCGGGGCG GCCAAACCAA TCGATGGCC GGGGCGGAGT CGGGCGCTCT
-30 ATAAGTTGTC GATGGGCGGG CACTCCGCCC TAGTTTCTAA GGATCATGTC
+20 TGCGAGCCAG GATTCCCG